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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=9; day=3; hr=7; min=25; sec=46; ms=165; ]

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Application No: 10586499 Version No: 2.0

Input Set:

Output Set:

Started: 2009-08-19 17:04:20.657  
Finished: 2009-08-19 17:04:21.522  
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 865 ms  
Total Warnings: 6  
Total Errors: 2  
No. of SeqIDs Defined: 7  
Actual SeqID Count: 7

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 323	Invalid/missing amino acid numbering SEQID (2)at Protein (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 323	Invalid/missing amino acid numbering SEQID (3)at Protein (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)

# SEQUENCE LISTING

<110> ITOH, Kyogo  
SHICHIJO, Shigeki

<120> Epidermal growth factor receptor (EGFR)-derived peptides

<130> 547586

<140> 10586499

<141> 2009-08-19

<150> JP 2004-015676

<151> 2004-01-23

<160> 7

<170> PatentIn version 3.2

<210> 1

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<212> PRT

<213> Artificial Sequence

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<223> EGFR-derived peptide at position 800-809.

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Asp Tyr Val Arg Glu His Lys Asp Asn Ile

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<223> EGFR-derived peptide at position 124-132.

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<212> PRT

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<223> EGFR-derived peptide at position 54-62.

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Met Phe Asn Asn Cys Glu Val Val Leu

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<212> PRT  
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<223> EGFR-derived peptide at position 479-488.

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<223> EGFR-derived peptide at position 1138-1147.

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<212> PRT  
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35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn  
50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys  
65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val  
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr  
100 105 110

Tyr	Glu	Asn	Ser	Tyr	Ala	Leu	Ala	Val	Leu	Ser	Asn	Tyr	Asp	Ala	Asn	115	120	125	
Lys	Thr	Gly	Leu	Lys	Glu	Leu	Pro	Met	Arg	Asn	Leu	Gln	Glu	Ile	Leu	130	135	140	
His	Gly	Ala	Val	Arg	Phe	Ser	Asn	Asn	Pro	Ala	Leu	Cys	Asn	Val	Glu	145	150	155	160
Ser	Ile	Gln	Trp	Arg	Asp	Ile	Val	Ser	Ser	Asp	Phe	Leu	Ser	Asn	Met	165	170	175	
Ser	Met	Asp	Phe	Gln	Asn	His	Leu	Gly	Ser	Cys	Gln	Lys	Cys	Asp	Pro	180	185	190	
Ser	Cys	Pro	Asn	Gly	Ser	Cys	Trp	Gly	Ala	Gly	Glu	Glu	Asn	Cys	Gln	195	200	205	
Lys	Leu	Thr	Lys	Ile	Ile	Cys	Ala	Gln	Gln	Cys	Ser	Gly	Arg	Cys	Arg	210	215	220	
Gly	Lys	Ser	Pro	Ser	Asp	Cys	Cys	His	Asn	Gln	Cys	Ala	Ala	Gly	Cys	225	230	235	240
Thr	Gly	Pro	Arg	Glu	Ser	Asp	Cys	Leu	Val	Cys	Arg	Lys	Phe	Arg	Asp	245	250	255	
Glu	Ala	Thr	Cys	Lys	Asp	Thr	Cys	Pro	Pro	Leu	Met	Leu	Tyr	Asn	Pro	260	265	270	
Thr	Thr	Tyr	Gln	Met	Asp	Val	Asn	Pro	Glu	Gly	Lys	Tyr	Ser	Phe	Gly	275	280	285	
Ala	Thr	Cys	Val	Lys	Lys	Cys	Pro	Arg	Asn	Tyr	Val	Val	Thr	Asp	His	290	295	300	
Gly	Ser	Cys	Val	Arg	Ala	Cys	Gly	Ala	Asp	Ser	Tyr	Glu	Met	Glu	Glu	305	310	315	320
Asp	Gly	Val	Arg	Lys	Cys	Lys	Lys	Cys	Glu	Gly	Pro	Cys	Arg	Lys	Val	325	330	335	
Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu	Ser	Ile	Asn	340	345	350	
Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile	Ser	Gly	Asp	355	360	365	
Leu	His	Ile	Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe	Thr	His	Thr	370	375	380	
Pro	Pro	Leu	Asp	Pro	Gln	Glu	Leu	Asp	Ile	Leu	Lys	Thr	Val	Lys	Glu	385	390	395	400
Ile	Thr	Gly	Phe	Leu	Leu	Ile	Gln	Ala	Trp	Pro	Glu	Asn	Arg	Thr	Asp	405	410	415	

Leu	His	Ala	Phe	Glu	Asn	Leu	Glu	Ile	Ile	Arg	Gly	Arg	Thr	Lys	Gln	
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His	Gly	Gln	Phe	Ser	Leu	Ala	Val	Val	Ser	Leu	Asn	Ile	Thr	Ser	Leu	
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Gly	Leu	Arg	Ser	Leu	Lys	Glu	Ile	Ser	Asp	Gly	Asp	Val	Ile	Ile	Ser	
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Gly	Asn	Lys	Asn	Leu	Cys	Tyr	Ala	Asn	Thr	Ile	Asn	Trp	Lys	Lys	Leu	
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Phe	Gly	Thr	Ser	Gly	Gln	Lys	Thr	Lys	Ile	Ile	Ser	Asn	Arg	Gly	Glu	
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Asn	Ser	Cys	Lys	Ala	Thr	Gly	Gln	Val	Cys	His	Ala	Leu	Cys	Ser	Pro	
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Glu	Gly	Cys	Trp	Gly	Pro	Glu	Pro	Arg	Asp	Cys	Val	Ser	Cys	Arg	Asn	
			515						520						525	
Val	Ser	Arg	Gly	Arg	Glu	Cys	Val	Asp	Lys	Cys	Lys	Leu	Leu	Glu	Gly	
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Glu	Pro	Arg	Glu	Phe	Val	Glu	Asn	Ser	Glu	Cys	Ile	Gln	Cys	His	Pro	
545						550						555			560	
Glu	Cys	Leu	Pro	Gln	Ala	Met	Asn	Ile	Thr	Cys	Thr	Gly	Arg	Gly	Pro	
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Lys	Tyr	Ala	Asp	Ala	Gly	His	Val	Cys	His	Leu	Cys	His	Pro	Asn	Cys	
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Thr	Tyr	Gly	Cys	Thr	Gly	Pro	Gly	Leu	Glu	Gly	Cys	Pro	Thr	Asn	Gly	
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Pro	Lys	Ile	Pro	Ser	Ile	Ala	Thr	Gly	Met	Val	Gly	Ala	Leu	Leu	Leu	
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Ile	Val	Arg	Lys	Arg	Thr	Leu	Arg	Arg	Leu	Leu	Gln	Glu	Arg	Glu	Leu	
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Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly	Glu	Ala	Pro	Asn	Gln	Ala	Leu	Leu	
690						695						700				
Arg	Ile	Leu	Lys	Glu	Thr	Glu	Phe	Lys	Lys	Ile	Lys	Val	Leu	Gly	Ser	
705						710						715			720	

Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Leu	Trp	Ile	Pro	Glu	Gly	Glu	
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Lys	Val	Lys	Ile	Pro	Val	Ala	Ile	Lys	Glu	Leu	Arg	Glu	Ala	Thr	Ser	
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Pro	Lys	Ala	Asn	Lys	Glu	Ile	Leu	Asp	Glu	Ala	Tyr	Val	Met	Ala	Ser	
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Val	Asp	Asn	Pro	His	Val	Cys	Arg	Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser	
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Thr	Val	Gln	Leu	Ile	Thr	Gln	Leu	Met	Pro	Phe	Gly	Cys	Leu	Leu	Asp	
785					790					795					800	
Tyr	Val	Arg	Glu	His	Lys	Asp	Asn	Ile	Gly	Ser	Gln	Tyr	Leu	Leu	Asn	
				805					810					815		
Trp	Cys	Val	Gln	Ile	Ala	Lys	Gly	Met	Asn	Tyr	Leu	Glu	Asp	Arg	Arg	
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Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Lys	Thr	Pro	
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Gln	His	Val	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Ala	Lys	Leu	Leu	Gly	Ala	
	850					855					860					
Glu	Glu	Lys	Glu	Tyr	His	Ala	Glu	Gly	Gly	Lys	Val	Pro	Ile	Lys	Trp	
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Met	Ala	Leu	Glu	Ser	Ile	Leu	His	Arg	Ile	Tyr	Thr	His	Gln	Ser	Asp	
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Val	Trp	Ser	Tyr	Gly	Val	Thr	Val	Trp	Glu	Leu	Met	Thr	Phe	Gly	Ser	
			900					905					910			
Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Ala	Ser	Glu	Ile	Ser	Ser	Ile	Leu	Glu	
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Lys	Gly	Glu	Arg	Leu	Pro	Gln	Pro	Pro	Ile	Cys	Thr	Ile	Asp	Val	Tyr	
	930					935					940					
Met	Ile	Met	Val	Lys	Cys	Trp	Met	Ile	Asp	Ala	Asp	Ser	Arg	Pro	Lys	
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Phe	Arg	Glu	Leu	Ile	Ile	Glu	Phe	Ser	Lys	Met	Ala	Arg	Asp	Pro	Gln	
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Arg	Tyr	Leu	Val	Ile	Gln	Gly	Asp	Glu	Arg	Met	His	Leu	Pro	Ser	Pro	
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Thr	Asp	Ser	Asn	Phe	Tyr	Arg	Ala	Leu	Met	Asp	Glu	Glu	Asp	Met	Asp	
		995					1000					1005				
Asp	Val	Val	Asp	Ala	Asp	Glu	Tyr	Leu	Ile	Pro	Gln	Gln	Gly	Phe	Phe	
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Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu Ser Ala  
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Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn Gly Leu Gln  
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Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg Tyr Ser Ser Asp  
1060 1065 1070

Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp Asp Thr Phe Leu Pro  
1075 1080 1085

Val Pro Glu Tyr Ile Asn Gln Ser Val Pro Lys Arg Pro Ala Gly Ser  
1090 1095 1100

Val Gln Asn Pro Val Tyr His Asn Gln Pro Leu Asn Pro Ala Pro Ser  
1105 1110 1115 1120

Arg Asp Pro His Tyr Gln Asp Pro His Ser Thr Ala Val Gly Asn Pro  
1125 1130 1135

Glu Tyr Leu Asn Thr Val Gln Pro Thr Cys Val Asn Ser Thr Phe Asp  
1140 1145 1150

Ser Pro Ala His Trp Ala Gln Lys Gly Ser His Gln Ile Ser Leu Asp  
1155 1160 1165

Asn Pro Asp Tyr Gln Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn  
1170 1175 1180

Gly Ile Phe Lys Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val  
1185 1190 1195 1200

Ala Pro Gln Ser Ser Glu Phe Ile Gly Ala  
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<210> 7

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<212> PRT

<213> Artificial Sequence

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<223> HIV peptide with HLA-A24 binding motif

<400> 7

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